

Mutation sequence analysis

Contributed by : CHU Lille

HGVS nomenclature (NM_000295.4)

Nomenclature including the signal peptide

c.250G>A

Type of variation	Mutation Location	Genetic background	ACMG classification
AAT variant	Exon 2	M1	Uncertain significance

Comments

rs111850950

AAT variant and Q0 alleles

Variant name	Also Known as	Pathogenicity	HGVS nomenclature protéine
M _{6passau}		Unknown	p.Ala84Thr
3D position of aa affected	Mobility on polyacrylamide gel		Mobility on agarose gel
			M
AATserum level (g/L)		Anti-elastolytic activity (IU/L)	
Heterozygous	Homozygous	Heterozygous	Homozygous
1.17		18290	

Comments

associated with a M1 allele.

Occurrence

Ethnic background without frequency range :

Ethnic background and frequency

Frequency range		Group tested			
from (%)	To (%)	Size	Description (who was tested)		
0.02	0.06				
Occurrence comments					
from gnomAD (2.1)					
Overall comments					
Occurrence comments					
This variant was identified at a heterozygous status in a 45-year old man presenting with bronchiectasis and a severe pulmonary obstruction.					
References n°1					
Medline ID	Authors		Title		
27296815	Silva D,Oliveira MJ,Guimarães M,Lima R,Gomes S,Seixas S		Alpha-1-antitrypsin (SERPINA1) mutation spectrum: Three novel variants and haplotype characterization of rare deficiency alleles identified in Portugal.		
Journal		Year	Volume	Num	Pp
Respiratory medicine		2016	116		8-18
References n°2					
Medline ID	Authors		Title		
7977369	Faber JP,Poller W,Weidinger S,Kirchgesser M,Schwaab R,Bidlingmaier F,Olek K		Identification and DNA sequence analysis of 15 new alpha 1-antitrypsin variants, including two PI*Q0 alleles and one deficient PI*M allele.		
Journal		Year	Volume	Num	Pp
American journal of human genetics		1994	55	6	1113-21
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